

ABSTRACT

The invention provides a mass analysis method and apparatus capable of identifying proteins or peptides at greater speed and with improved accuracy. Specifically, a mass analysis method whereby a sample is ionized and a protein is analyzed using a mass analysis apparatus is provided, said method comprising: selecting predetermined information from a database in which information about proteins and peptides is stored, estimating the mass of the selected component, and calculating frequency information for each mass; analyzing a sample using a mass analysis apparatus so as to acquire a mass spectrum, selecting, based on the acquired mass spectrum and said frequency information, a mass to be used for identification, performing mass analysis using the mass spectrum of the selected mass as a precursor ion, and performing an identification process using a resultant mass spectrum. The method allows a precursor ion for obtaining an MS/MS spectrum required for identification processing to be efficiently selected using the frequency information matched with the purpose of analysis.